AMENDMENTS TO THE CLAIMS

1.-35. (Canceled)

36. (Currently Amended) A method for identifying a compound which binds to a ~~preselected~~ ~~biomolecular~~ nucleic acid target comprising at least one loop, bulge, kink, stem structure, or mismatched base pair, said compound being present in a mixture of compounds, comprising:

(a) providing a complex of said ~~biomolecular~~ nucleic acid target and a standard binding compound which binds to said target under conditions effective to achieve said binding;

(b) combining with said complex under competitive binding conditions the mixture of compounds;

(c) ionizing said combination in a mass spectrometer to provide a plurality of ions;

(d) fragmenting at least one of said ions in a mass spectrometer, (e) collecting mass spectral data for the fragmentation; and

(f) relating said mass spectral data to the existence and degree of competitive binding.

37. (Canceled)

38. (Currently Amended) The method of claim [[37]] 36 wherein said nucleic acid is RNA.

39. (Original) The method of claim 38 wherein said RNA includes one or more deoxynucleotides at preselected locations thereof.

40. (Canceled)

41. (Currently Amended) A method for identifying a compound which binds to a ~~preselected~~ ~~biomolecular~~ nucleic acid target comprising at least one loop, bulge, kink, stem structure, or mismatched base pair, said compound being present in a mixture of compounds, comprising:

(a) providing a complex of said ~~biomolecular~~ nucleic acid target and a standard compound which binds to said target under conditions effective to achieve said binding;

(b) acquiring fragmentation data from the mass spectrometric analysis of the complex;

(c) combining with a further portion of said complex under competitive binding conditions the mixture of compounds;

(d) ionizing said combination in a mass spectrometer to provide a plurality of ions;

(e) fragmenting at least one of said ions in a mass spectrometer;

(f) collecting mass spectral data for the fragmentation; and (g) relating the mass spectral data acquired in steps (b) and (f) to the existence and degree of competitive binding of said compound.

42. (Currently Amended) A method for identifying in a combinatorial mixture compounds which bind to a ~~biomolecular~~ nucleic acid target comprising at least one loop, bulge, kink, stem structure, or mismatched base pair, wherein the method comprises:

(a) providing mass spectral data on the ion abundance for said ~~biomolecular~~ nucleic acid target;

(b) providing a first complex of said ~~biomolecular~~ nucleic acid target and a standard binding compound which binds to said target;

(c) combining with said first complex a combinatorial mixture of compounds;

(d) ionizing in a mass spectrometer said combination from step ~~(circle over (c))~~ (c) to provide a plurality of ions for said combination;

(e) collecting from the ionization of step (d) mass spectral data on the ion abundance of said first complex, wherein said ion abundances in steps (a) and (e) affords information for effecting said determination.

43. (Original) The method of claim 42 wherein mass differences in the mass spectral data from steps (a) and (e) are identified for determining the mass of compounds from the combinatorial mixture which preferentially bind with said bimolecular target.

44. (Canceled)

45. (Currently Amended) The method of claim [[44]] 42 wherein said nucleic acid is RNA.

46. (Original) The method of claim 45 wherein said RNA corresponds to a 16S rRNA A-site.

47. (Original) The method of claim 45 wherein said RNA includes one or more deoxynucleotide subunits at preselected locations thereof.

48. - 94. (Canceled)

95. (Previously Presented) The method of claim 36, wherein said compound is an oligonucleotide.

96. (Canceled)

97. (Currently Amended) The method of claim [[38]] 36, wherein said compound is a small molecule.

98. (Previously Presented) The method of claim 38, wherein said RNA comprises a molecular interaction site present in two or more distinct taxonomic species.

99. (Previously Presented) The method of claim 41, wherein said compound is an oligonucleotide.

100. (Canceled)

101. (Currently Amended) The method of claim 41, wherein said nucleic acid is RNA.

102. (Canceled)

103. (Previously Presented) The method of claim 101, wherein said RNA comprises a molecular interaction site present in two or more distinct taxonomic species.

104. (Previously Presented) The method of claim [[100]] 41, wherein said compound is a small molecule.

105. (Previously Presented) The method of claim 42, wherein said compound is an oligonucleotide.

106. (Canceled)

107. (Previously Presented) The method of claim 45, wherein said RNA comprises a molecular interaction site present in two or more distinct taxonomic species.

108. (Currently Amended) The method of claim [[45]] 42, wherein said compound is a small molecule.

109. (New) The method of claim 38, wherein said RNA comprises a molecular interaction site.

110. (New) The method of claim 101, wherein said RNA comprises a molecular interaction site.

111. (New) The method of claim 45, wherein said RNA comprises a molecular interaction site.

AMENDMENTS TO THE DRAWINGS

Please delete Figures 1, 4, 5, 7-12, 24, and 27 of the application as filed containing the Drawings and insert substitute Figures 1, 4, 5, 7-12, 24, and 27 enclosed herewith.